

Leu Ser Pro Gly	Ala Thr Val Ala Leu	Leu Leu Pro Ala Gly	Pro
215		220	225
Glu Phe Leu Trp	Leu Trp Phe Gly Leu	Ala Lys Ala Gly Leu	Arg
230		235	240
Thr Ala Phe Val	Pro Thr Ala Leu Arg	Arg Gly Pro Leu Leu	His
245		250	255
Cys Leu Arg Ser	Cys Gly Ala Arg Ala	Leu Val Leu Ala Pro	Glu
260		265	270
Phe Leu Glu Ser	Leu Glu Pro Asp Leu	Pro Ala Leu Arg Ala	Met
275		280	285
Gly Leu His Leu	Trp Ala Ala Gly Pro	Gly Thr His Pro Ala	Gly
290		295	300
Ile Ser Asp Leu	Leu Ala Glu Val Ser	Ala Glu Val Asp Gly	Pro
305		310	315
Val Pro Gly Tyr	Leu Ser Ser Pro Gln	Ser Ile Thr Asp Thr	Cys
320		325	330
Leu Tyr Ile Phe	Thr Ser Gly Thr Thr	Gly Leu Pro Lys Ala	Ala
335		340	345
Arg Ile Ser His	Leu Lys Ile Leu Gln	Cys Gln Gly Phe Tyr	Gln
350		355	360
Leu Cys Gly Val	His Gln Glu Asp Val	Ile Tyr Leu Ala Leu	Pro
365		370	375
Leu Tyr His Met	Ser Gly Ser Leu Leu	Gly Ile Val Gly Cys	Met
380		385	390
Gly Ile Gly Ala	Thr Val Val Leu Lys	Ser Lys Phe Ser Ala	Gly
395		400	405
Gln Phe Trp Glu	Asp Cys Gln Gln His	Arg Val Thr Val Phe	Gln
410		415	420
Tyr Ile Gly Glu	Leu Cys Arg Tyr Leu	Val Asn Gln Pro Pro	Ser
425		430	435
Lys Ala Glu Arg	Gly His Lys Val Arg	Leu Ala Val Gly Ser	Gly
440		445	450
Leu Arg Pro Asp	Thr Trp Glu Arg Phe	Val Arg Arg Phe Gly	Pro
455		460	465
Leu Gln Val Leu	Glu Thr Tyr Gly Leu	Thr Glu Gly Asn Val	Ala
470		475	480
Thr Ile Asn Tyr	Thr Gly Gln Arg Gly	Ala Val Gly Arg Ala	Ser
485		490	495
Trp Leu Tyr Lys	His Ile Phe Pro Phe	Ser Leu Ile Arg Tyr	Asp

Val Thr Thr Gly	Glu Pro Ile Arg Asp	Pro Gln Gly His Cys Met
515	520	525
Ala Thr Ser Pro	Gly Glu Pro Gly Leu	Leu Val Ala Pro Val Ser
530	535	540
Gln Gln Ser Pro	Phe Leu Gly Tyr Ala	Gly Gly Pro Glu Leu Ala
545	550	555
Gln Gly Lys Leu	Leu Lys Asp Val Phe	Arg Pro Gly Asp Val Phe
560	565	570
Phe Asn Thr Gly	Asp Leu Leu Val Cys	Asp Asp Gln Gly Phe Leu
575	580	585
Arg Phe His Asp	Arg Thr Gly Asp Thr	Phe Arg Trp Lys Gly Glu
590	595	600
Asn Val Ala Thr	Thr Glu Val Ala Glu	Val Phe Glu Ala Leu Asp
605	610	615
Phe Leu Gln Glu	Val Asn Val Tyr Gly	Val Thr Val Pro Gly His
620	625	630
Glu Gly Arg Ala	Gly Met Ala Ala Leu	Val Leu Arg Pro Pro His
635	640	645
Ala Leu Asp Leu	Met Gln Leu Tyr Thr	His Val Ser Glu Asn Leu
650	655	660
Pro Pro Tyr Ala	Arg Pro Arg Phe Leu	Arg Leu Gln Glu Ser Leu
665	670	675
Ala Thr Thr Glu	Thr Phe Lys Gln Gln	Lys Val Arg Met Ala Asn
680	685	690
Glu Gly Phe Asp	Pro Ser Thr Leu Ser	Asp Pro Leu Tyr Val Leu
695	700	705
Asp Gln Ala Val	Gly Ala Tyr Leu Pro	Leu Thr Thr Ala Arg Tyr
710	715	720
Ser Ala Leu Leu	Ala Gly Asn Leu Arg	Ile
725	730	

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- <211> 22
- <212> DNA
- <213> Artificial Sequence
- <220>
- <223> Synthetic oligonucleotide probe
- <400> 103
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<212> DNA  
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<220>  
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<212> DNA  
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<223> Synthetic oligonucleotide probe

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<212> DNA  
<213> Homo sapiens

<400> 108  
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cctccacgca cacacatccc caagaacctc gagctcacac caacagacac 100  
acgcgcgcac acacactcgc tctcgtttgt ccatctccct cccgggggag 150  
ccggcgcgcg ctcccacctt tgccgcacac tccggcgagc cgagcccgca 200